

Expected Fragment Sizes (kb)		
using Probe A		
Restriction Digest	Fragment Length wild type	mutant

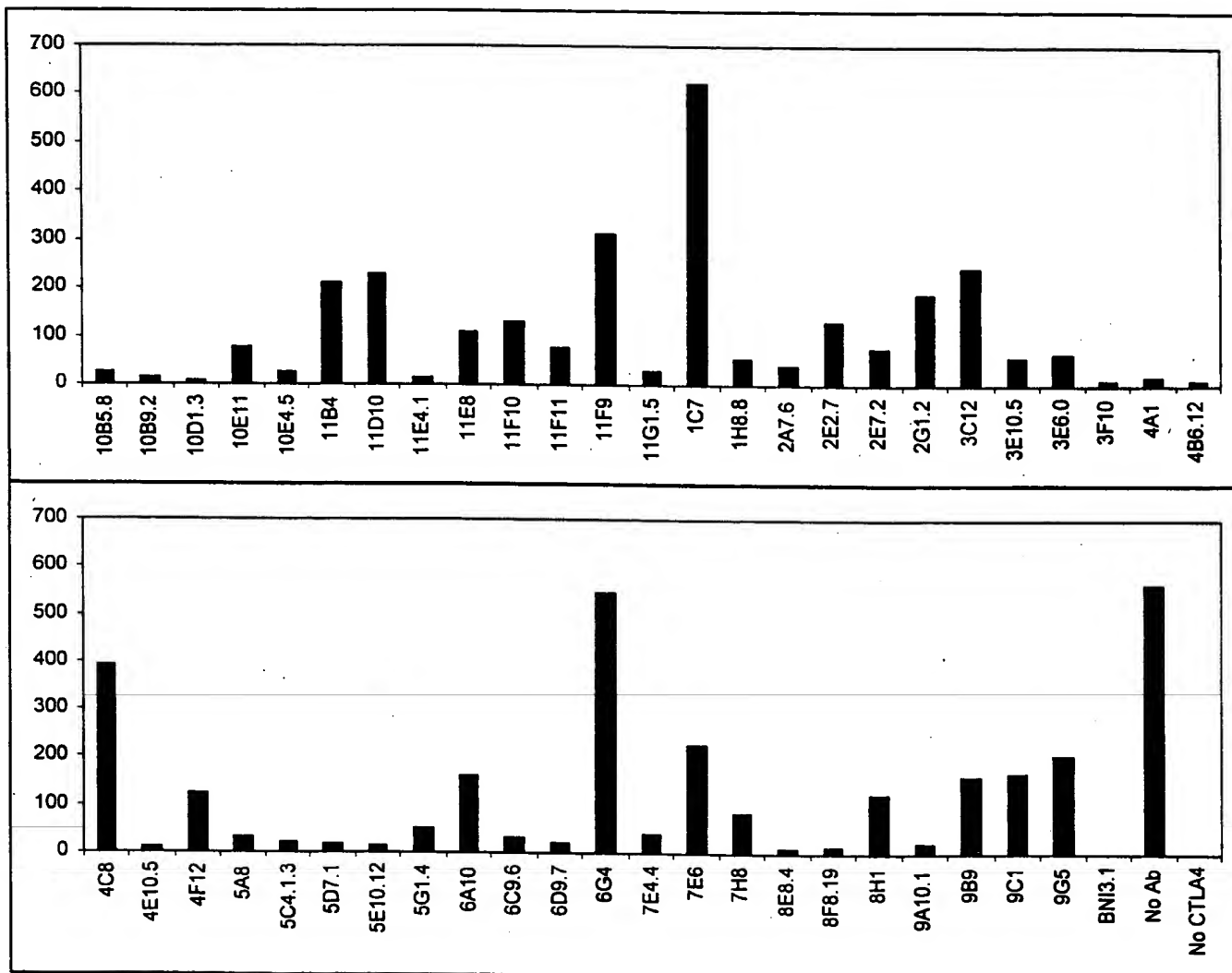
Bgl I	15.7	7.7
Bst XI	7.3	6.6
Spe I	9.9	7.6
Eco RI	12.5	14.3

FIG. 1

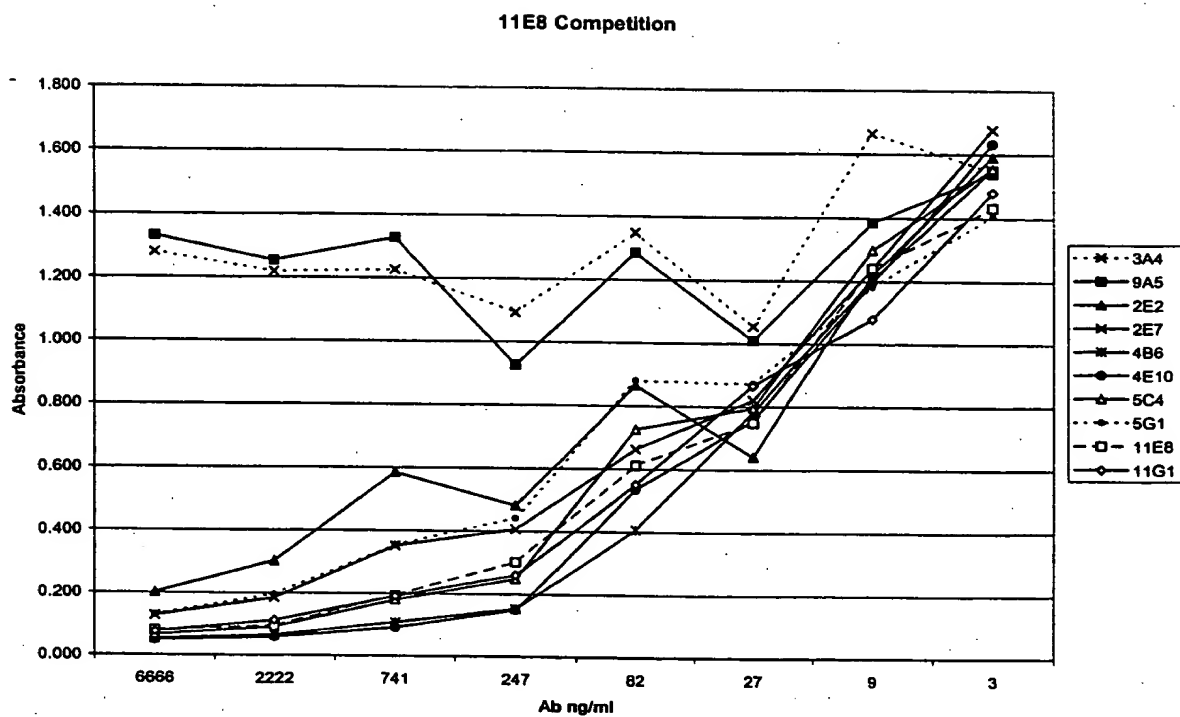
05644568.082400

004220" 89944960

**FIGURE 2**



**FIGURE 3**



004280" 89944960

### 10D1.3 VH (SEQ ID NO:2)

TGGGGGAGGC GTGGTCCAGC CTGGGAGGTC CCTGAGACTC TCCTGTGCAG 50  
CCTCTGGATT CACCTTCAGT AGCTATACTA TGCACTGGGT CCGCCAGGCT 100  
CCAGGCAAGG GGCTGGAGTG GGTGACATTT ATATCATATG ATGGAAACAA 150  
TAAATACTAC GCAGACTCCG TGAAGGGCCG ATTCACCATC TCCAGAGACA 200  
ATTCCAAGAA CACGCTGTAT CTGCAAATGA ACAGCCTGAG AGCTGAGGAC 250  
ACGGCTATAT ATTACTGTGC GAGGACCGGC TGGCTGGGGC CCTTTGACTA 300  
CTGGGGCCAG GGAACCCTGG TCACCGTCTC CTCAGCCTCC ACCAAGGGC 349

### 10D1.3 VK (SEQ ID NO:3)

CTCCAGGCAC CCTGTCTTTG TCTCCAGGGG AAAGAGCCAC CCTCTCCTGC 50  
AGGGCCAGTC AGAGTGTTGG CAGCAGCTAC TTAGCCTGGT ACCAGCAGAA 100  
ACCTGGCCAG GCTCCCAGGC TCCTCATCTA TGGTGCATTC AGCAGGGCCA 150  
CTGGCATCCC AGACAGGTTC AGTGGCAGTG GGTCTGGGAC AGACTTCACT 200  
CTCACCATCA GCAGACTGGA GCCTGAAGAT TTTGCAGTGT ATTACTGTCA 250  
GCAGTATGGT AGCTCACCGT GGACGTTCGG CCAAGGGACC AAGGTGGAAA 300  
TCAAACGAAC TGTGGCTGCA C 321

Figure 4

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V<sub>K</sub> A-27  
 Germline:  
 10D1:  
 4B6:

V<sub>K</sub> A-27:  
 10D1:  
 4B6:

V<sub>K</sub> A-27:  
 10D1:  
 4B6:

V<sub>K</sub> A-27:  
 10D1:  
 4B6:

V<sub>K</sub> A-27:  
 10D1:  
 4B6:

V<sub>K</sub> L-15  
 Germline:  
 1E2:

V<sub>K</sub> L-15:  
 1E2:

V<sub>K</sub> L-15:  
 1E2:

V<sub>k</sub> L-15:  
1E2:

GAT TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT GAA GAT TTT GCA ACT TAT TAC TGC CAA CAG TAT AAT  
-----  
CDR3

V<sub>k</sub> L-15:  
1E2:

AGT TAC CCT CC  
-----  
J<sub>k1</sub>  
--G ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C/

FIG. 5

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V<sub>H</sub> 3-30.3  
 Germline:  
 10D1:  
 4B6:

CAG	GTG	CAG	CTG	GTG	GAG	TCT	GGG	GGA	GGC	GTG	GTC	CAG	CCT	GGG	AGG	TCC	CTG	AGA	CTC	TCT	GCA	GCC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

V<sub>H</sub> 3-30.3:  
 10D1:  
 4B6:

TCT	GGA	TTC	ACC	TTC	AGT	AGC	TAT	GCT	ATG	CAC	TGG	GTC	CGC	CAG	GCT	CCA	GGC	AAG	GGG	CTG	GAG	TGG	GTG
---	---	---	---	---	---	---	---	A-	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
---	---	---	---	---	---	---	A-	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

V<sub>H</sub> 3-30.3:  
 10D1:  
 4B6:

GCA	GTT	ATA	TCA	TAT	GAT	GGA	AGC	AAT	AAA	TAC	TAC	GCA	GAC	TCC	GTG	AAG	GGC	CGA	TTC	ACC	ATC	TCC	AGA
A--	T--	---	---	---	---	---	---	A-	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
A--	T--	---	---	---	---	---	---	---	---	C--	---	---	---	---	---	---	---	---	---	---	G--	---	---

V<sub>H</sub> 3-30.3:  
 10D1:  
 4B6:

GAC	AAT	TCC	AAG	AAC	ACG	CTG	TAT	CTG	CAA	ATG	AAC	AGC	CTG	AGA	GCT	GAG	GAC	ACG	GCT	GTG	TAT	TAC	TGT
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	A-A	---	---	---
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

V<sub>H</sub> 3-30.3:  
 10D1:  
 4B6:

GCG	AGA	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

V<sub>H</sub> 3-33  
 Germline:  
 1E2:

CAG	GTG	CAG	CTG	GTG	GAG	TCT	GGG	GGA	GGC	GTG	GTC	CAG	CCT	GGG	AGG	TCC	CTG	AGA	CTC	TCC	TGT	GCA	GCG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

V<sub>H</sub> 3-33:  
 1E2:

TCT	GGA	TTC	ACC	TTC	AGT	AGC	TAT	GGC	ATG	CAC	TGG	GTC	CGC	CAG	GCT	CCA	GGC	AAG	GGG	CTG	GAG	TGG	GTG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

V<sub>H</sub> 3-33:  
 1E2:

GCA	GTT	ATA	TGG	TAT	GAT	GGA	AGT	AAT	AAA	TAC	TAT	GCA	GAC	TCC	GTG	AAG	GGC	CGA	TTC	ACC	ATC	TCC	AGA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

FIG. 6  
 102

V<sub>H</sub> 3-33: GAC AAT TCC AAG AAC ACG CTG TAT CTG CAA ATG AAC AGC CTG AGA GCC GAG GAC ACG GCT GTG TAT TAC TGT  
1E2: ----- -T- -----

CDR3  
J<sub>H</sub>3b

V<sub>H</sub> 3-33: GCC AGA GA  
1E2: -----CT CCC AAT TAT ATT GGT GCT TTT GAT GTC TGG GGC CAA GGG ACA ATG GTC ACC GTC TCT TCA G/

FIG. 6

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V<sub>K</sub> A-27  
 Germline:  
 10D1:  
 4B6:

	_____CDR1_____	_____CDR2_____
EIVLTQSPGTLSPGERATLSC	RASQSVSSSYLA	WYQOKPGQAPRLIY GASSRAT
-----G-----		-----F-----
-----F-----		

V<sub>K</sub> A-27:  
 10D1:  
 4B6:

	_____CDR3_____
GIPDRFSGSGGTDFLTISRLEPEDFAVYYC	QQYCSS
-----PWT	FGQGTKEVEIK
-----	

V<sub>K</sub> L-15  
 Germline:  
 1E2:

	_____CDR1_____	_____CDR2_____
DIQMTQSPSSLASVGDRTITC	RASQGISWLA	WYQOKPEKAPKSLIY AASSLQS
-----		

V<sub>K</sub> L-15:  
 1E2:

	_____CDR3_____
GVPDRFSGSGGTDFLTISLQPEDFATYYC	QQYNSY
-----PPT	FGQGTKEVEIK
-----	

FIG. 7

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V<sub>H</sub> 3-30.3  
 Germline:  
 10D1:  
 4B6:

QVQVLESGGGVQPGRSRLRLSCAASGFTFS	SYAMH	WVRQAPGKLEWVA	VISYDGSNKYYADSVKG
-----	-T-	-----	F-----N-----
-----	-T-	-----	F-----H-----

CDR1

CDR2

CDR3

V<sub>H</sub> 3-30.3:  
 10D1:  
 4B6:

RFTISRDN SKNTLYLQMSLRAEDTAVYYCAR	TGWLGPFDY	WGQGTLLVTSS
-----I-----	-----	-----
---V-----I---	-----	-----

V<sub>H</sub> 3-33  
 Germline:  
 1E2:

QVQVLESGGGVQPGRSRLRLSCAASGFTFS	SYGMH	WVRQAPGKLEWVA	VIWYDGSNKYYADSVKG
-----	-----	-----	-----

CDR1

CDR2

CDR3

V<sub>H</sub> 3-33:  
 1E2:

RFTISRDN SKNTLYLQMSLRAEDTAVYYCAR	APNYIGAFDV	WGQGTMTVSS
-----F-----	-----	-----

FIG. 8

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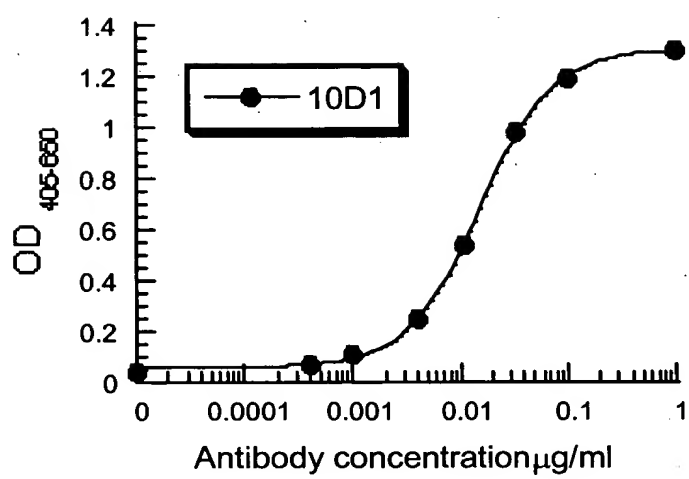


Figure 9

004280" 39944960

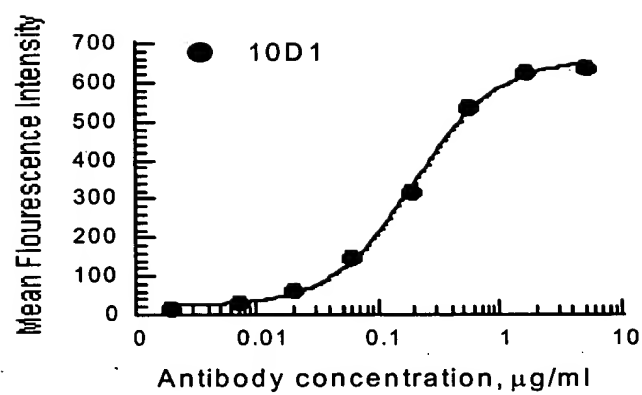


Figure 10

0944660 084400

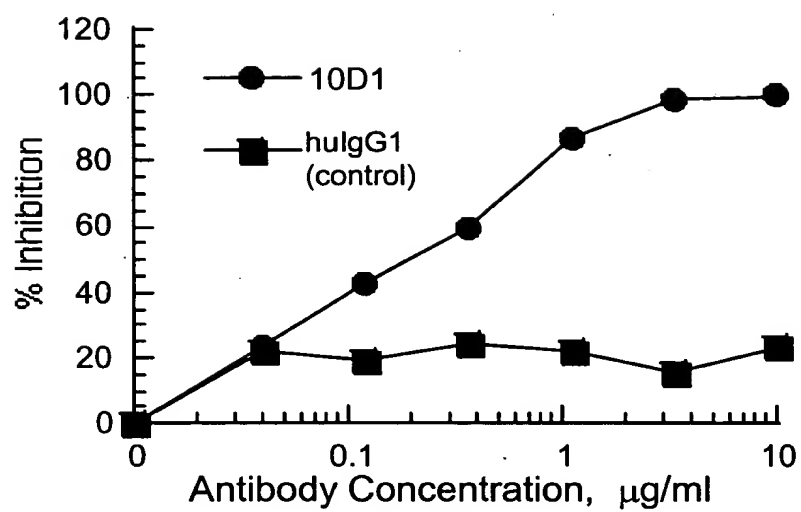


Figure 11.

004280" 8994960

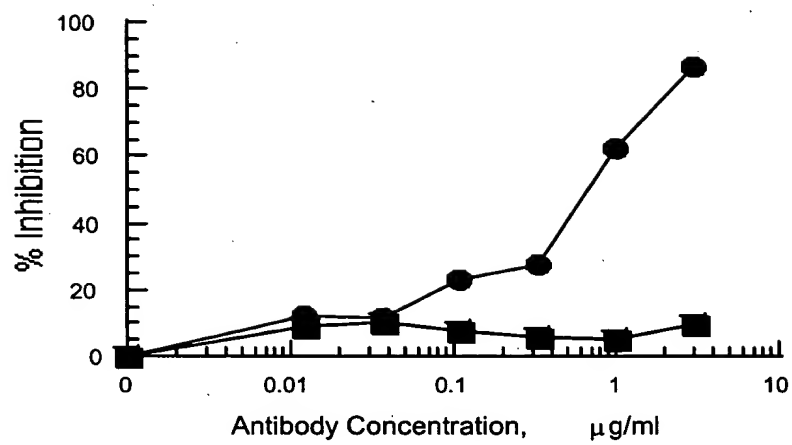


Figure 12

004280" 89944960

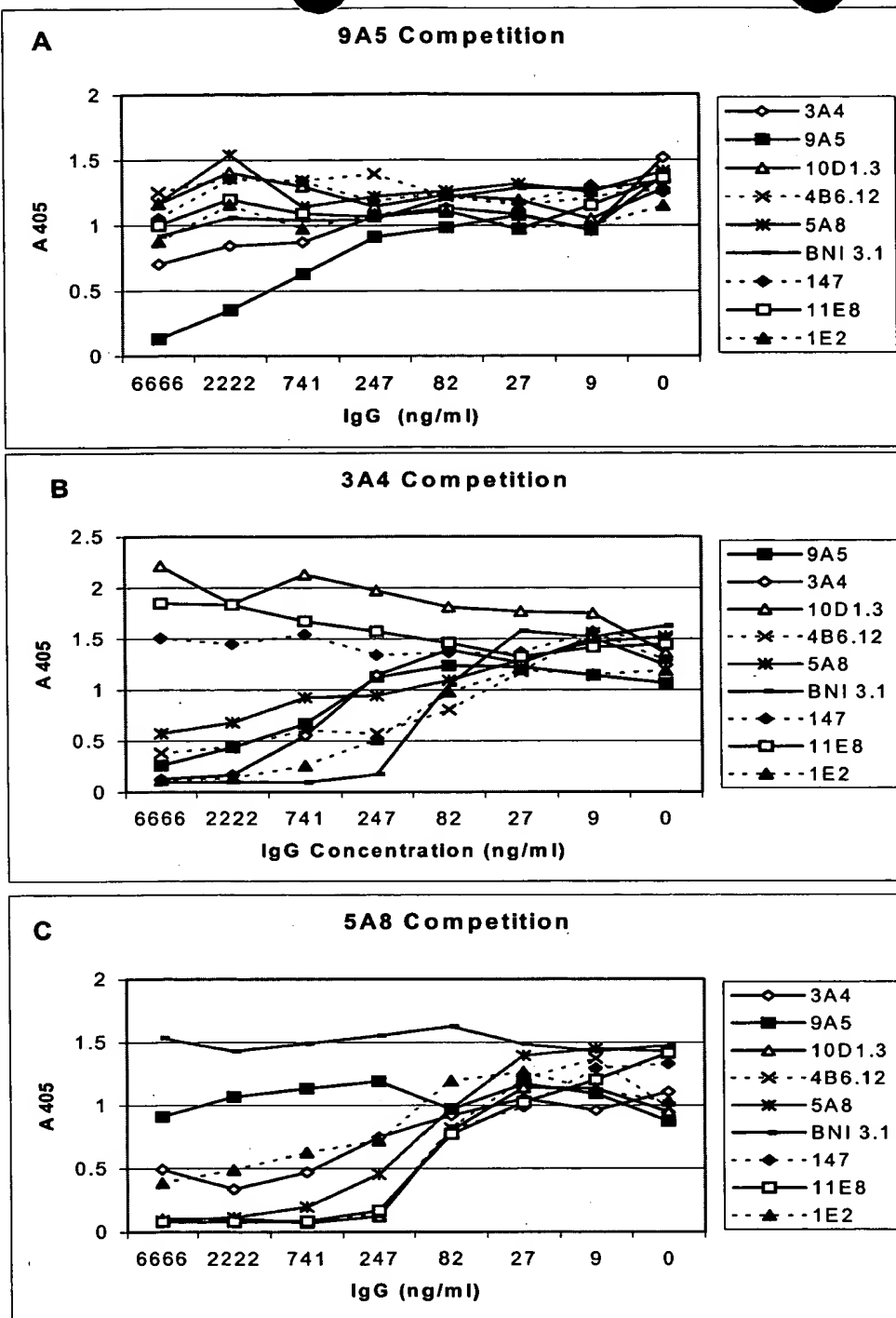


Figure 13A-13C

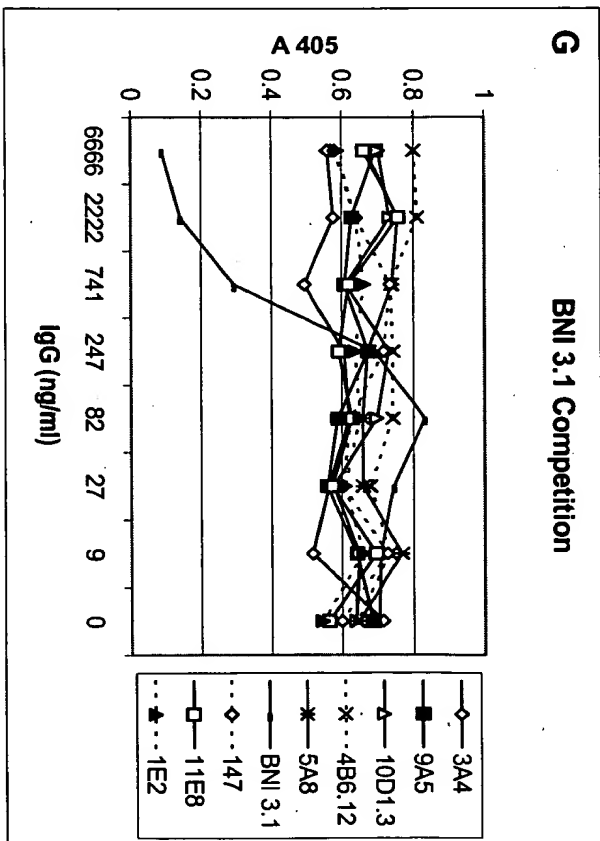
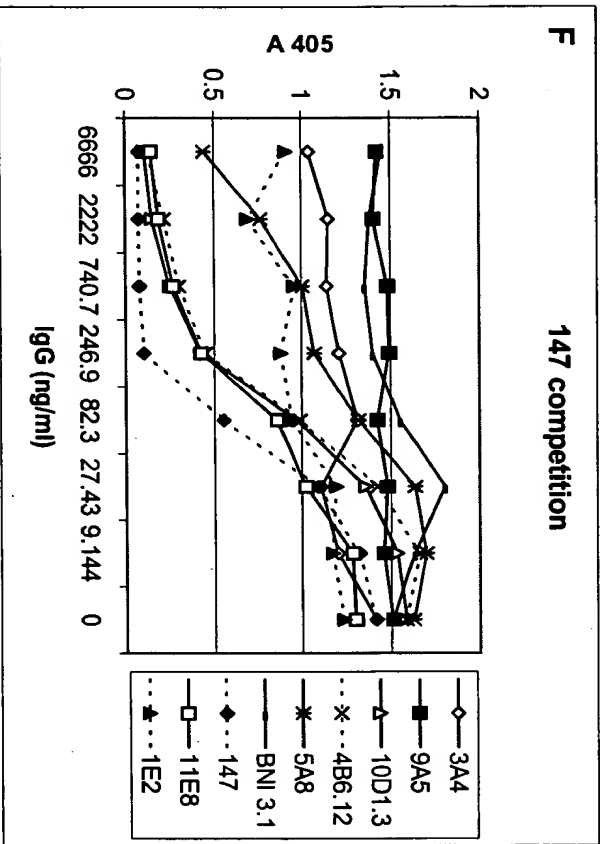
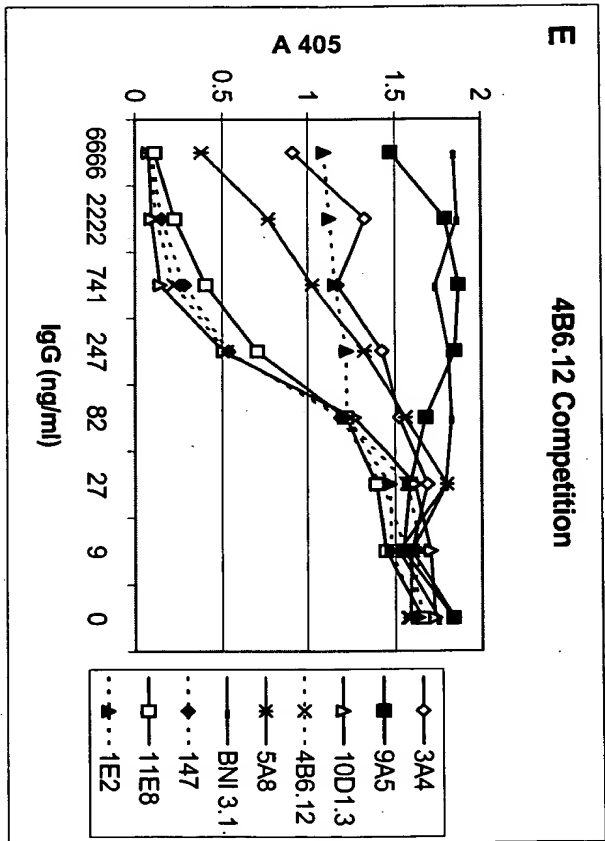
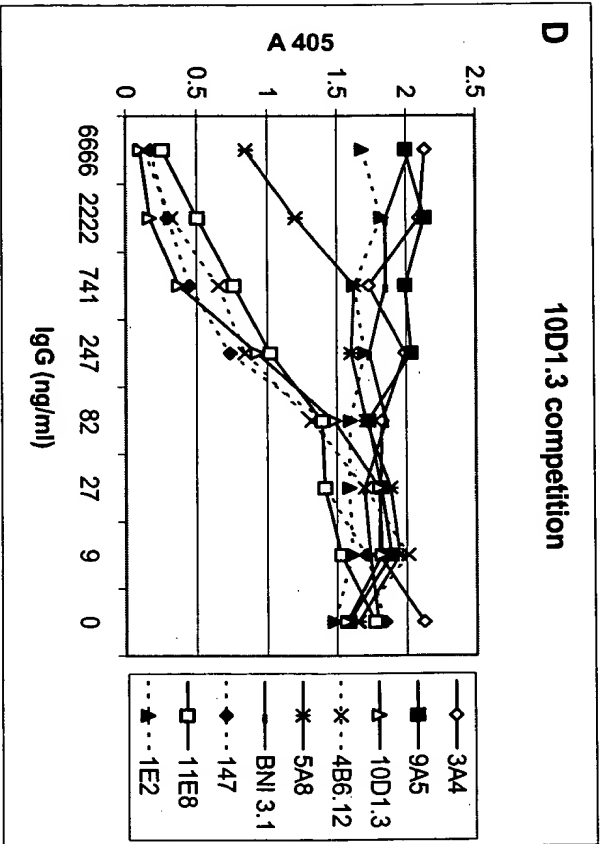
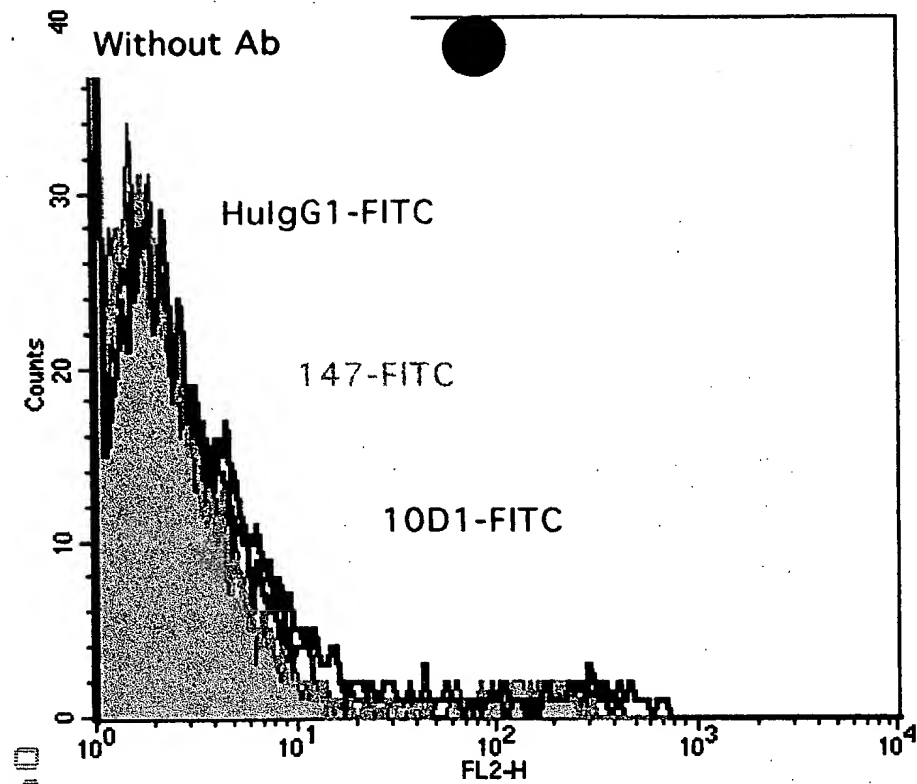


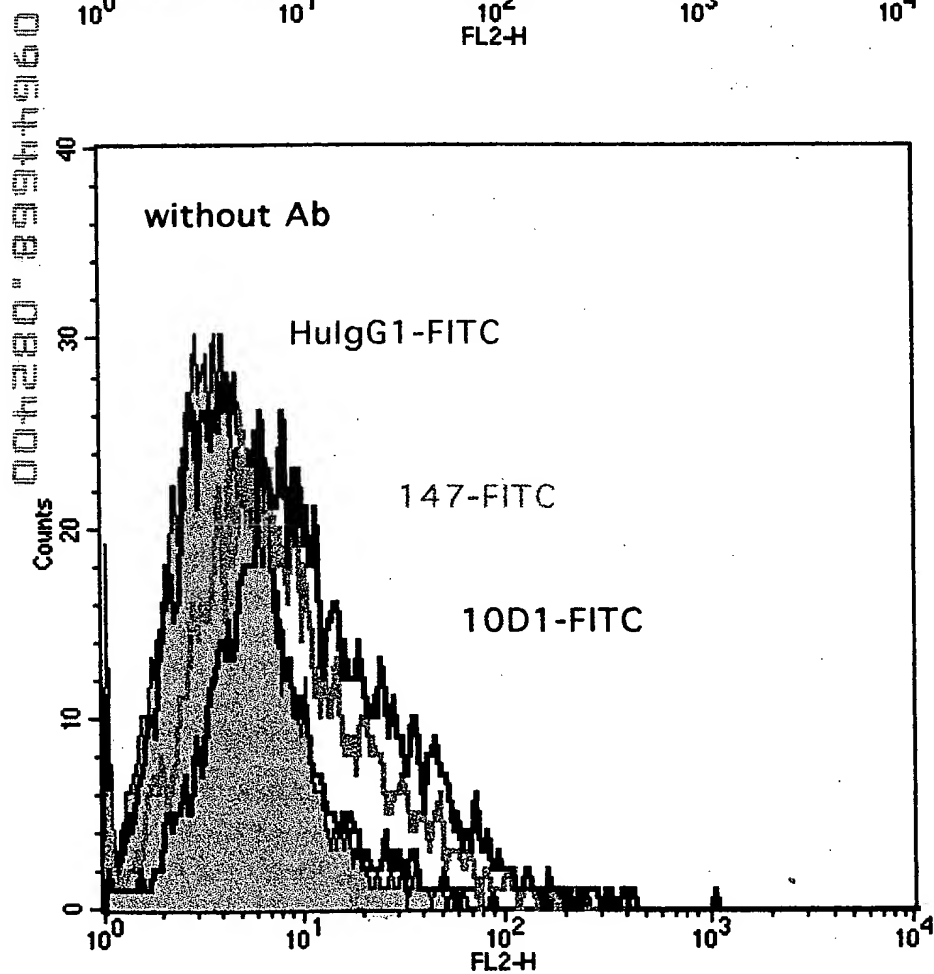
Figure 13D-13G

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Control lymphocytes



PHA activated  
lymphocytes

10D1 Application  
FIG. 14

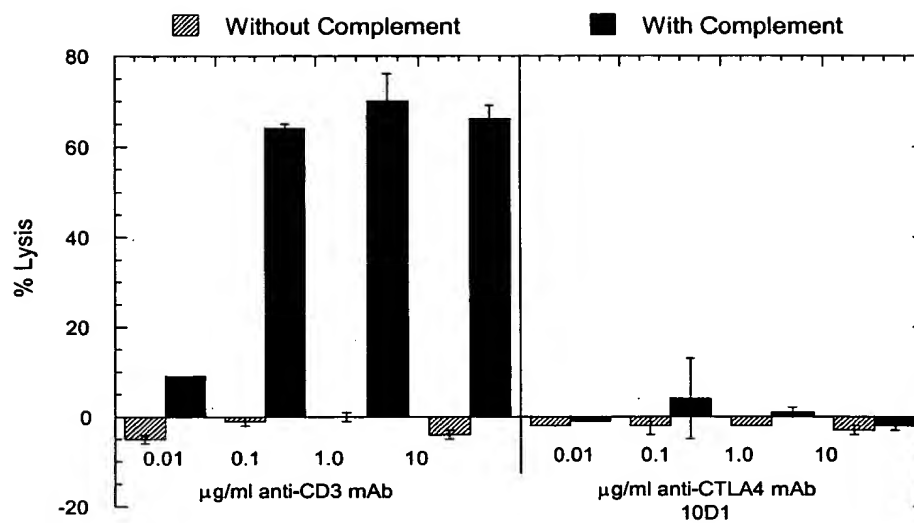


Figure 15

004280"89944950

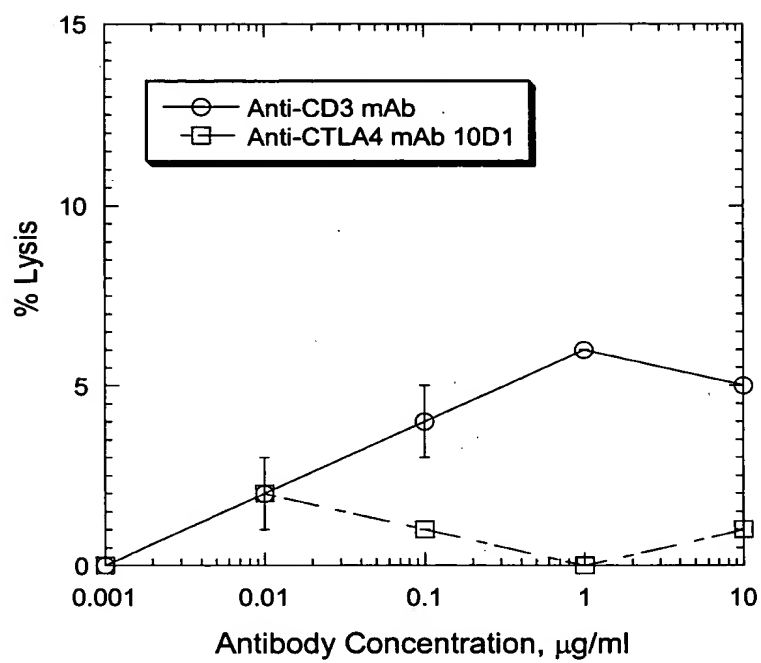


Figure 16.

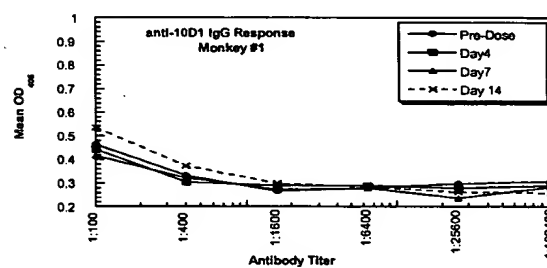
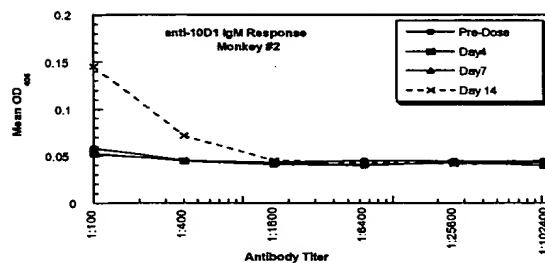
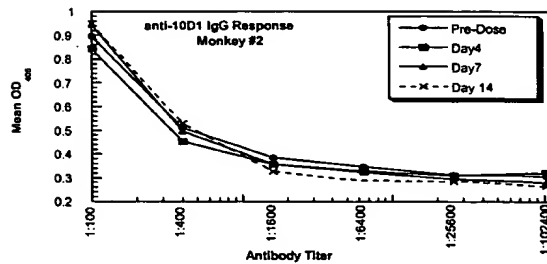
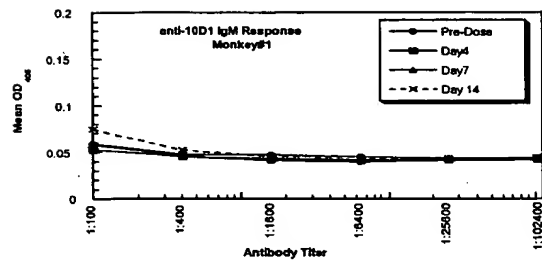


Figure 17

Study No. MDXCTLA4-01																				
Selected Lab Values Summary																				
						PSA														
Screen no.	Subject no.	Initials	Amendment #	Day	Date	ng/ml	Platelets	WBC	Neuts	Lymphs	Monos	Eos	CD4	CD8	ESR	Hgb	Hct			
						x10 <sup>9</sup> /L	x10 <sup>9</sup> /L	%	%	%	%	%	/L	/L	mm/hr	g/dl	%			
02001	001	JGR	Scr			144.80	263	8.12	73.00	5.90	18.00	1.47	5.60	0.46	1.80	0.15	670	367	71	
02001	001	JGR	0			185.20	267	5.74	66.00	3.79	22.00	1.32	6.60	0.38	3.10	0.18	704	376		
02001	001	JGR	1			259	259	6.31	69.00	4.38	20.00	1.29	8.70	0.55	0.90	0.06	A	A		
02001	001	JGR	2			240	240	6.59	70.00	4.66	19.00	1.31	6.70	0.44	1.80	0.12	556	303		
02001	001	JGR	3			270	270	6.53	71.00	4.63	21.00	1.36	5.50	0.36	2.20	0.14	608	254		
02001	001	JGR	7			257.40	299	6.70	68.00	4.56	23.00	1.53	6.00	0.40	2.50	0.17	A	A		
02001	001	JGR	14			332.30	308	6.87	71.90	7.94	21.20	1.39	5.21	0.36	1.90	0.13	A	A		
02001	001	JGR	21			285	286	9.72	74.00	7.20	19.70	1.91	4.80	0.46	1.00	0.10	A	A		
02001	001	JGR	28			351.00	304	5.38	63.00	3.40	26.00	1.44	5.80	0.31	2.90	0.16	A	A		
01002		JWF	Scr			28.30	271	11.60	75.40	8.75	13.60	1.58	5.70	0.66	4.60	0.53	399	189	41	
01003		MZB	Scr			12.70	178	5.49	69.00	3.79	19.60	1.08	6.30	0.35	2.70	0.24	325	168	19	
01004		TEQ	Scr			1459.00	264	6.26	75.10	4.70	14.40	0.90	7.70	0.48	2.40	0.15	365	129	61	
01005		WVN	Scr			182.40	212	6.85	73.70	5.05	17.40	1.20	6.20	0.43	2.20	0.15	483	217		
01006		MRS	Scr			4503.00	140	7.55	76.70	5.79	15.90	1.20	6.20	0.47	0.80	0.06	319	363	83	
01007		TAB	Scr			1394.00	205	5.78	73.00	4.24	13.00	0.76	6.50	0.37	6.00	0.35	376	127		
01008		CHB	Scr			70.70	229	4.67	54.00	2.56	32.00	1.52	8.30	0.39	3.40	0.16	461	499		
01009	003	RAB	Scr			238.60	144	3.70	78.00	2.88	14.00	0.55	5.40	0.20	1.20	0.04	211	162	43	
01009	003	RAB	0			336.90	123	3.92	68.00	2.67	21.00	0.83	8.70	0.34	1.50	0.06	374	188		
01009	003	RAB	1			122	122	3.35	71.00	2.38	22.00	0.74	4.00	0.14	1.80	0.06	307	192		
01009	003	RAB	2			109	109	4.05	74.00	2.99	19.00	0.77	4.80	0.20	1.20	0.05	328	220		
01009	003	RAB	3			114	114	3.79	70.00	2.67	21.00	0.81	6.20	0.23	1.30	0.05	313	265		
01009	003	RAB	7			249.30	69	3.38	75.00	2.54	17.00	0.60	5.60	0.19	0.70	0.02	244	161		
01009	003	RAB	14			269.80	101	3.68	69.00	2.54	21.20	0.78	8.50	0.31	1.00	0.04	308	173		
01009	003	RAB	21			122	122	4.82	78.00	3.76	13.20	0.64	7.70	0.37	0.60	0.03	218	195		
01012	004	CEH	Scr			112.90	172	5.85	64.00	3.74	28.00	1.69	5.60	0.33	1.00	0.06	746	451	10	
01012	004	CEH	1			150	150	4.82	67.70	3.26	26.40	1.28	4.60	0.22	1.10	0.05	552	380		
01012	004	CEH	2			147	147	4.36	63.70	2.78	29.30	1.28	5.10	0.22	1.30	0.06	544	441		
01012	004	CEH	3			190.00	159	4.95	58.60	2.90	32.70	1.61	5.90	0.29	2.50	0.12	842	506		
01012	004	CEH	14			207.60	189	5.64	63.10	3.55	29.30	1.65	5.70	0.32	1.60	0.09				
01013		KJF	Scr			49.10	228	8.53	65.00	5.62	26.00	2.23	5.30	0.46	2.30	0.20	1213	398		
02014	002	L-S	Scr			12.70	222	5.65	53.00	3.01	34.00	1.92	7.40	0.42	3.90	0.22	721	439		
02014	002	L-S	0			27.50	217	5.88	57.00	3.36	32.00	1.88	8.60	0.50	1.50	0.09	676	389		
02014	002	L-S	1			226	226	5.74	55.00	3.19	35.00	2.04	7.00	0.40	1.40	0.08	632	405		
02014	002	L-S	2			223	223	5.58	55.00	3.09	32.00	1.84	9.80	0.55	1.40	0.08	590	339		
02014	002	L-S	3			219	219	4.89	54.00	2.66	34.00	1.68	7.50	0.37	2.70	0.13	529	358		
01016	Reliable	G-F	Scr			4856.00	106	7.31	86.00	6.29	5.00	0.33	6.80	0.49	1.90	0.14	578	7		
					low	7.00	150	3.80	40.50	1.96	15.40	0.80	2.80	0.12	6.60	0.57	1612	1129	30	
					high			10.70	75.00	7.23	48.50	3.00	10.10	0.92	6.80	0.57	1612	1129		

TABLE 11

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2

Study No. MDXCTLA4-02																			
Selected Lab Values Summary																			
							WBC	Neuts	Lymphs	Monos	Eos	CD4	CD8	ESR	Hgb	Hct			
Screen no.	Subject no.	Initials	Amendment #	Day	Date	x10 <sup>9</sup> /L	x10 <sup>9</sup> /L	%	x10 <sup>9</sup> /L	%	x10 <sup>9</sup> /L	%	x10 <sup>9</sup> /L	%	g/dl	%			
02001	001	SAH	0	Scr		216	6.28	56.60	3.52	35.60	2.23	5.90	0.37	1.80	0.11	1189	631	14.4	39
02001	001	SAH	0	0		230	5.58	59.70	3.33	32.30	1.80	5.70	0.32	1.80	0.10	1039	502	14.9	43
02001	001	SAH	0	1		202	5.12	61.80	3.16	30.20	1.55	5.00	0.26	2.30	0.12	957	407	13.4	37
			normal range		low	150	3.90	40.50	1.96	15.40	0.80	2.60	0.12			404	220		
					high		10.70	75.00	7.23	48.50	3.00	10.10	0.92	6.80	0.57	1612	1129	30	

TABLE 13

09644668 . 082400